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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/903,023

DATE: 10/30/2001
 TIME: 12:01:27

Input Set : A:\Rih32d11.app
 Output Set: N:\CRF3\10302001\I903023.raw

3 <110> APPLICANT: Wands, Jack R.
 4 de la Monte, Suzanne M.
 5 Ince, Nedim
 6 Carlson, Rolf I.
 8 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
 10 <130> FILE REFERENCE: 21486-032 DIV1
 12 <140> CURRENT APPLICATION NUMBER: 09/903,023
 C--> 13 <141> CURRENT FILING DATE: 2001-10-11 *09*
 15 <150> PRIOR APPLICATION NUMBER: 09/436,184
 16 <151> PRIOR FILING DATE: 1999-11-08
 18 <160> NUMBER OF SEQ ID NOS: 9
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 36
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus ✓
 29 EGF-like domain
 31 <220> FEATURE:
 32 <221> NAME/KEY: VARIANT
 33 <222> LOCATION: (2)..(8)
 34 <223> OTHER INFORMATION: Wherein Xaa is any amino acid ✓
 36 <220> FEATURE:
 37 <221> NAME/KEY: VARIANT
 38 <222> LOCATION: (10)..(13)
 39 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
 41 <220> FEATURE:
 42 <221> NAME/KEY: VARIANT
 43 <222> LOCATION: (15)..(24)
 44 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
 46 <220> FEATURE:
 47 <221> NAME/KEY: VARIANT
 48 <222> LOCATION: (26)
 49 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
 51 <220> FEATURE:
 52 <221> NAME/KEY: VARIANT
 53 <222> LOCATION: (28)..(35)
 54 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
 56 <400> SEQUENCE: 1
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 58 1 5 10 15
 W--> 60 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa 30
 61 20 25 30
 W--> 63 Xaa Xaa Xaa Cys
 64 35
 67 <210> SEQ ID NO: 2

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Input Set : A:\Rih32d11.app
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68 <211> LENGTH: 758
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 2
73 Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser
74 1 5 10 15
76 Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
77 20 25 30
79 Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
80 35 40 45
82 Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
83 50 55 60
85 Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
86 65 70 75 80
88 Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
89 85 90 95
91 Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
92 100 105 110
94 Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
95 115 120 125
97 Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
98 130 135 140
100 Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
101 145 150 155 160
103 Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
104 165 170 175
106 Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
107 180 185 190
109 Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
110 195 200 205
112 Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
113 210 215 220
115 Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
116 225 230 235 240
118 Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
119 245 250 255
121 Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
122 260 265 270
124 Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
125 275 280 285
127 Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
128 290 295 300
130 Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
131 305 310 315 320
133 Glu Gln Lys Ala Lys Val Lys Lys Lys Pro Lys Leu Leu Asn Lys
134 325 330 335
136 Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
137 340 345 350
139 Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val

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140	355	360	365
142	Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys		
143	370	375	380
145	Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly		
146	385	390	395
148	400	405	410
149	415		
151	Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe		
152	420	425	430
154	Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln		
155	435	440	445
157	Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr		
158	450	455	460
160	Leu Leu Ile Gly Asp Asn Asp Ala Lys Lys Val Tyr Glu Glu Val		
161	465	470	475
163	480	485	490
164	495		
166	Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys		
167	500	505	510
169	Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr		
170	515	520	525
172	Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr		
173	530	535	540
175	Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp		
176	545	550	555
178	560	565	570
179	575		
181	Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg		
182	580	585	590
184	Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala		
185	595	600	605
187	Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp		
188	610	615	620
190	Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala		
191	625	630	635
193	640	645	650
194	655		
196	Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro		
197	660	665	670
199	Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg		
200	675	680	685
202	Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys		
203	690	695	700
205	Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp		
206	705	710	715
208	720	725	730
209	735		
211	Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg		
212	740	745	750

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214 Arg Ser Leu Pro Ala Ile
215 755
218 <210> SEQ ID NO: 3
219 <211> LENGTH: 2324
220 <212> TYPE: DNA
221 <213> ORGANISM: Homo sapiens
223 <400> SEQUENCE: 3
224 cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacacgc agcagcagcgc 60
225 gctccggcag cggtgcacg agtgcggca gcagcagccc cggggcccg agagagacaa 120
226 agcatggagg acacaagaat gggaggaaag gcggactctc gggacttca ttcttcacgt 180
227 ggttatggt gattgcattt ctggcgctt ggacatctgt agctgtcggt tgggttgc 240
228 ttgttgcata tgaggaagtt ctaggaaaac taggaatcta tgatgtcgat ggtgtatggag 300
229 attttgatgt ggatgtatgc aaagttttat taggacttaa agagagatct acttcagagc 360
230 cagcagtccc gccagaagag gctgagccac acactgagcc cgaggagcag gttcctgtgg 420
231 aggccagaacc ccagaatatac gaagatgaag caaaagaaca aattcagttc ctttcctatg 480
232 aaatggtaca cgcagaacat gttgaggggag aagacttgc acaagaagat ggaccacag 540
233 gagaaccaca acaagaggat gatgagtttcc ttatggcgac tgatgttagat gatagatttgc 600
234 agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtgaaagaga 660
235 cagtttcaca agactgtat caggatatgg aagagatgtat gtctgagcag gaaaatcccg 720
236 attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtacat 780
237 accaagtcta tgaggaacaa gcagtatatg aacctctaga aatgaaggg atagaaatca 840
238 cagaagtaac tgctccccctt gaggataatc ctgtagaaga ttccacagta attttagaa 900
239 aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaaa 960
240 cagatgatcc agaacaaaaaa gcaaaaagtta agaaaaagaa gcctaaactt taaaataat 1020
241 ttgataagac tattaaagct gaacttgcattt ctgcagaaaa actccgtaaa agggaaaaaa 1080
242 ttgaggaagc agtgaatgc tttaaagaaac tagtacgaa ataccctcag agtccacag 1140
243 caagatatgg gaaggcgcag tttgaggatg atttggctga gaagaggaga agtaatgagg 1200
244 tgctacgtgg agccatcgag accttaccaag aggtggccag cctacctgat gtccctgcag 1260
245 acctgctgaa gctgagtttgc aagcgtcgct cagacaggca acaatttcta ggtcatatgc 1320
246 gaggttccctt gcttaccctg cagagatttttgc ttcactatt tcccaatgtat acttcctt 1380
247 aaaatgaccc tggcgtggaa taccttcttgc taggagataa tgacaatgc aagaaagttt 1440
248 atgaagaggt gctgagtgta acacctaatttgc atggcttgc taaagtccat tatggcttca 1500
249 tcctgaaggc acagaacaaa attgctgaga gcatccccata tttaaagaa ggaatagaat 1560
250 ccggagatcc tggcactgtat gatgggagat tttatttccat cctggggat gccatgcaga 1620
251 gggttggaa caaagaggca tataagtggat atgagcttgg gcacaagaga ggacactttg 1680
252 catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttgggtgg 1740
253 ccccaaaaaga aacggcgtac acagagtttgc taaaagtctt agaaagaaaac tggaaatggaa 1800
254 tccgagatgc aggccttgc gtttatggata aagccaaagg tctttccat cctggggat 1860
255 aaaacctgag ggaaaaaggactggagcc agttcacgtt gtggcagca ggaagaagaa 1920
256 atgaaaatgc ctgcaaaaggat gctccctaaaaa cctgtacctt actagaaaaag ttccccgaga 1980
257 caacaggatg cagaagagga cagatcaatatttgc atccatcat gcaccccccgg actcacgtgt 2040
258 gggccgcacac agggccacaca aactgcaggc tccgaatgc cctgggtttgc gtgattccca 2100
259 aggaaggctg caagattcga tttgtccaaacg agaccaggac ctggggagaa ggcaaggtgc 2160
260 tcatactttgc tgactccattt gggcacgagg tatggcaggat gtcctcatct ttccgggtgc 2220
261 tatttcattgttgc ggtatgtgtgg catccggaaac tgacaccaca gcagagacgc agccttccag 2280
262 caattttagca tgaattcatgc caagcttggg aaactctggaa gaga 2324
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 31
267 <212> TYPE: PRT

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Input Set : A:\Rih32d11.app
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268 <213> ORGANISM: Artificial Sequence
 270 <220> FEATURE:
 271 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF-like
 272 cysteine-rich repeat
 274 <220> FEATURE:
 275 <221> NAME/KEY: VARIANT
 276 <222> LOCATION: (3)..(5)
 277 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid
 279 <220> FEATURE:
 280 <221> NAME/KEY: VARIANT
 281 <222> LOCATION: (6)..(7)
 282 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 284 <220> FEATURE:
 285 <221> NAME/KEY: VARIANT
 286 <222> LOCATION: (10)
 287 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 289 <220> FEATURE:
 290 <221> NAME/KEY: VARIANT
 291 <222> LOCATION: (14)
 292 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 294 <220> FEATURE:
 295 <221> NAME/KEY: VARIANT
 296 <222> LOCATION: (17)..(18)
 298 <220> FEATURE:
 299 <221> NAME/KEY: VARIANT
 300 <222> LOCATION: (25)..(26)
 301 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 303 <220> FEATURE:
 304 <221> NAME/KEY: VARIANT
 305 <222> LOCATION: (29)
 306 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 308 <400> SEQUENCE: 4
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 310 5 10 15
 W--> 312 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys 618
 313 20 25 30
 316 <210> SEQ ID NO: 5
 317 <211> LENGTH: 1242
 318 <212> TYPE: PRT
 319 <213> ORGANISM: Homo sapiens
 321 <400> SEQUENCE: 5
 322 Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val
 323 1 5 10 15
 325 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
 326 20 25 30
 328 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
 329 35 40 45
 331 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
 332 50 55 60

VERIFICATION SUMMARY
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Input Set : A:\Rih32d11.app
Output Set: N:\CRF3\10302001\I903023.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4